

FIGURE 1

CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTTAAATATTTTAAATATT
AATATACATTTCTTCTGTCAGAAATACATAAACTTTATTATATCAGCGCAGG
5 GCGGCGCGGCGTCGGTCCCGGGAGCAGAACCCGGCTTTTTCTTGGAGCGACG
CTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTA
ATCTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCG
CATCCATCAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG
10 CTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTG
ACATGGCGGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACA
ATCAGTTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGT
GGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGACGATGGTGT
GGACACAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTTAAA
15 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTA
TTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGG
AATCTGTCACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACG
GATCCCCTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAGAATTTGATA
CAGTGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT
20 TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGAC
CGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA
GTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGC
CAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATT
GTGGCTGTGGAACCTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAC
25 CGTGAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGG
AGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATG
AACGATGTGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTGAGATAAG
AGACCCTTTTCTACCAGCAACCAAACCTTACTACTAGCCTGCAATGCAATGAA
30 CACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGA
AAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAATA

GTGTTTGAGGTTATATATGCACAAACACACACAGAAATATATTCATGTCTATG
TGTATATAGATCAAATGTTTTTTTTTGGTATATATAACCAGGTACACCAGAGCT
TACATATGTTTGAGTTAGACTCTTAAAATCCTTTGCCAAAATAAGGGATGGTC
AAATATATGAAACATGTCTTTAGAAAATTTAGGAGATAAATTTATTTTAAAT
5 TTTGAAACACAAAACAATTTTGAATCTTGCTCTCTTAAAGAAAGCATCTTGTA
TATTA AAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAGTTG (SEQ ID
NO:50)

FIGURE 2

1 CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTTAAAAATATTT
46 TAAATATTAATATACATTTCTTCTGTCAGAAATACATAAACTTT
5 91 ATTATATCAGCGCAGGGCGGCGCGGCGTCCGTCGGGAGCAGAA
136 CCCGGCTTTTTCTTGGAGCGACGCTGTCTCTAGTCGCTGATCCCA

181 AATGCACCGGCTCATCTTTGTCTACACTCTAATCTGCGCAAACCTT
MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe
10 226 TTGCAGCTGTCTGGGACACTTCTGCAACCCCGCAGAGCGCATCCAT
CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle

271 CAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
15 LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis
316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG
LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly

361 AAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAG
20 AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg
406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAATACACG
AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg
25 451 GATACAGCTAGTGTTTGACAATCAGTTTGGATTAGAGGAAGCAGA
IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu

496 AAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATC
30 AsnAspIleCysArgTyrAspPheValGluValGluAspIleSer
541 CGAAACCAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGA
GluThrSerThrIleIleArgGlyArgTrpCysGlyHisLysGlu

586 AGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTAAAATCAC
35 ValProProArgIleLysSerArgThrAsnGlnIleLysIleThr
631 ATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT
PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle
40 676 TTATTATTCTTTGCTGGAAGATTTCGAACCCGCAGCAGCTTCAGA
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu

721 GACCAACTGGGAATCTGTCACAAGCTCTATTTTCAGGGGTATCCTA
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

5 766 TAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGATGCTCT
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

811 GGACAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAA
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

10 856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

901 TCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAA
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA
SerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyr

20 991 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

1036 GAAGTTGGCCAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCA
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

25 1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGTCAACTGGAGGTC
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

1126 CTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGT
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

1171 ATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAA
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys

35 1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

40 1306 CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTG

1351 AGATAAGAGACCCTTTTCCTACCAGCAACCAAACCTTACTACTAGC

1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT

FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCAT
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA
10 GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTTG
GGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

15 EVQLVESGGGLVKPGGSLRLSCAASGFNFRITYNMNWVRQAPGKGLEWVSSISS
SSNIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIIAS
FYFDYWGQGLTVTVSS (SEQ ID NO:13)

20 C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TTTCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGA
ATCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:56)

30 D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTTCRASQGIRNDLGWFQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
ID NO:14)

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FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTTATA
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTC
CAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
10 GAGGACACGGCCGTGTATTACTGTGCGGGAACGGTGACTACGAATTACTACT
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

15 EVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG
GSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYYGM
DVWGQGTTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCAAAGTAATGGATAC
AACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAAGTGGCAGT
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
25 TTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCTCACTTTCGGCGGAGGG
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

30 DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLG
SNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTFGGGKVEI
K (SEQ ID NO:16)

FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGT
10 ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAAGGATACAGATATG
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:59)

15 B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGYRYA
GYYDYGM DVWGQGTTVTVSS (SEQ ID NO:17)

20 C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
25 TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:60)

30 D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
35 ID NO:18)

FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCAAACAGTGGTAACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGGTATAGCAGTGGC
TGGGACATACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:61)

15 B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTA YMELSSLRSED TAVYYCAREGIAVAG
TYYYYYGMDVWGQGTITVTVSS (SEQ D NO:19)

20 C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
25 TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTTCT
GTCTACAGCATAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:62)

30 D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ
35 ID NO:20)

FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAAC
CCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCA
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
10 ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTTG
GGGGAGTTATCGTGCACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARDVMITFG
GVIVHYGMDVWGQGTITVTVSS (SEQ ID NO:21)

20 C -- Cur2 1.19 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTGACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGA
GATCAGAC (SEQ ID NO:64)

30 D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTDFTLTISLQPEDFATYYCLQHNSDPCSFQGTGLEIR (SEQ
ID NO:22)

35

FIGURE 8

A -- Cur2 1.23 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG
TTTCGGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

15 EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYYVSGS
YYNVFDYWGGQGLTVTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGATACCAGGGAAAGCCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAACGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGA
ATCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
25 GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

30 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:24)

FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCAGTTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT
10 ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGGGATACAGCTATG
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:67)

15 B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVYYCARDQGYSYG
YVYYDYGMDVWGQGTITVTVSS (SEQ ID NO:25)

20 C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
25 TATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGA
GTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTCTGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:68)

30 D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
35 ID NO:26)

FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG
GTTTCGGAGACTTATTATAATGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSET
YYNVFDYWGGTGLTVSS (SEQ ID NO:27)

20 C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA
ATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:70)

30 D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:28)

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FIGURE 11

A -- Cur2 1.29 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGCCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGGCT
ACGATTGGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGGCCAAG
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG
DSDTRYSPSFQGGQATISADKSISTAYLQWSSLKASDTAMYICARHVDVGATIGG
YYYYYHGMDVWGQGTITVTVSS (SEQ ID NO:29)

20 C -- Cur2 1.29 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCCTGATC
25 TATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTTTGGCCA
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

30 D -- Cur2 1.29 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLG
SNRASGVPDRFSGSGSGTDFTLKISRVEADDVGIVYCMQALQSLMCSFGQGTKL
EIK (SEQ ID NO:30)

35

FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

5 CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
10 ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCATTACTATGATAGT
AGTGATTATCTCTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYDSS
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

20 C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCAC
25 TTTGCAATCAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAAAGTATAACAGTGCCCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGA
TCAAAC (SEQ ID NO:74)

30 D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQ
SGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYNAPLTFGGGTKVEIK (SEQ
ID NO:32)

35

FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGT
ATGATGGAAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
10 GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA
GTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

15 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWY
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS
DYLYYYYGMDVWGQGTITVTVSS (SEQ ID NO:33)

20 C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCCTAACCTCCTGATCTATGCTGCATCCAC
25 TTTGCAATCAGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATCTGGGACAGATT
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT
CAAAAGTGTAACAGTGCCCCGTGGACGTTTCGGCCAAGGGACCACGGTGGAG
ATCAAAC (SEQ ID NO:76)

30 D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASLTQ
SGVPSRFSGSGSGTDFSLTISSLQPEDVAAYYCQKCNSAPWTFGQGTVEIK (SEQ
ID NO:34)

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FIGURE 14

A -- Cur2 1.39.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAACAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA
ATTCGGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

15 EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGHIYPG
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYYNSGS
YYNVFDYWGQGTLLTVSS (SEQ ID NO:35)

20 C -- Cur2 1.39.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:78)

30 D -- Cur2 1.39.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:36)

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FIGURE 15

A -- Cur2 1.40.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCACTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCCTAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AGCTGCTACCACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSKKASGYTFTTYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDVAVYYCARDIVVVV
AATNYYNGMDVWGQGTITVTVSS (SEQ ID NO:37)

20

FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA
TGGTTACGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARGSGYSYG
YDYYYGMDVWGQGTITVTVSS (SEQ ID NO:38)

20 C -- Cur2 1.45 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAATTGCCGGGCGAGTCAGGGCATTAGCAATGATTTAGCCTGG
TATCAGCAGAAACCAGGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCA
25 CTTTGCAATTAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG
TCAAAAGTATAACAGTGCCCCATTCATTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:81)

30 D -- Cur2 1.45 light chain protein sequence

DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASLTQ
LGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPFTFGPGTKVDIK (SEQ
ID NO:39)

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FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAATGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AACTGCTACGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYSTSYDINWVRQATGQGLEWMGWM
NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT
ATDYYYGMDVWGQGTTVTVSS (SEQ ID NO:40)

20 C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATTTTTGCTGCATCCA
25 GTTTGCCAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA
ATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAGTGGTTACCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:83)

30 D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID
NO:41)

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FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

5 CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
10 ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGTTGAATATTACTATG
ATGGTAGTGGTTATTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYD
GSGYYYFDYWGGQGLTVTVSS (SEQ ID NO:42)

20 C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGTTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA
25 TTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTTGCATCTTACTATT
GTCAACAGTCTAACAGTTTCCCTCGGACGTTTCGGCCAAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:85)

30 D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASILQ
SGVPSRFSGSGSGTDFLTITSLQPEDFASYQCQSNSFPRTFGQGTKVEIK (SEQ
ID NO:43)

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FIGURE 19

A -- Cur2 1.49.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTGACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGATTTTCTGTGCGAGAATGAGGGATATAGTGGC
TACGAGCTATTACTACTTCTACGGTATGGACGTCTGGGGCCAAGGGACC
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYFCARMRDIVAT
SYYYFYGMVWGQGTITVTVSS (SEQ ID NO:44)

20 C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC
25 TATTTGGGTTCTAGTCGGGCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAACCTCTACAACTATCACCTTCGGCCAAGGGA
CACGACTGGAGATTAAAC (SEQ ID NO:87)

30 D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWYLLKPGQSPQLLIYLG
SSRASGVDPDRFSGSGSDFTLKISRVEAEDVGVYYCMQTLQTITFGQGRLEIK
(SEQ ID NO:45)

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FIGURE 20

A -- Cur2 1.51 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATGCCAAATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTTGA
GGAATTATCGGTATACAGGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGT
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDAKYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYICARHYDYVWRNY
RYTGWFDPWGQGLVTVSS (SEQ ID NO:46)

20 C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT
25 CCAACAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGAC
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATT
ACTGTCAGCAGTATGGTAGCTCACTATTCACCTTTCGGCCCTGGGACCAAAGTG
GATATCAAAC (SEQ ID NO:89)

30 D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK (SEQ
ID NO:47)

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FIGURE 21

A -- Cur2 6.4 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATAAAC
CCTAATAGTGGTAACACAGACTATGCACAGAAGTTCCAGGGCAGAGTCACCA
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
10 ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGCTTTGGATACAGCTAT
AATTACGACTACTATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY
DYYYGMDVWGQGTITVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

20 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGTAGTAGTTACTTAGCCT
GGTACCAGCAGAAGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC
CAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACA
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTA
CTGTCAGCAGTATGGTAGTTACCGTGCAGTTTTGGCCAGGGGACCAAGCTG
25 GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

30 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGTGLEIK (SEQ
ID NO:49)

FIGURE 22A

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0

FIGURE 22B

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0

FIGURE 23

Figure 23A

								Section 1
	(1)	1	10	20	30	40	51	
CUR2-1.6.1_HC	(1)	EVQLVESGGGLVKPGGSLRLSCAASGFNFR						TYMNNWVRQAPGKGLEWVSSI
VH3-21	(1)	EVQLVESGGGLVKPGGSLRLSCAASGFTFS						YSMNNWVRQAPGKGLEWVSSI
Consensus	(1)	EVQLVESGGGLVKPGGSLRLSCAASGF						F SY MNNWVRQAPGKGLEWVSSI
								Section 2
	(52)	52	60	70	80	90	102	
CUR2-1.6.1_HC	(52)	SSSSSNIIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMI						
VH3-21	(52)	SSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR----						
Consensus	(52)	SSSSS IYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR						
								Section 3
	(103)	103	110	126				
CUR2-1.6.1_HC	(103)	TFGGIIASFYFDYWGQGLTVTVSS						
VH3-21	(99)	-----						
Consensus	(103)							

Figure 23B

										Section 1
	(1)	1	10	20	30	40	51			
CUR2-1.6.1_LC	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI								RNDLGWFQQKPGKAPKRLIYAA
A30	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI								RNDLGWFQQKPGKAPKRLIYAA
Consensus	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI								RNDLGWFQQKPGKAPKRLIYAA
										Section 2
	(52)	52	60	70	80	90	102			
CUR2-1.6.1_LC	(52)	SSLQSGVPSRFSGSGSGTEFTLT								ISSLPQEDFATYYCLOHNSYPLTFGGGT
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLT								ISSLPQEDFATYYCLOHNSYP-----
Consensus	(52)	SSLQSGVPSRFSGSGSGTEFTLT								ISSLPQEDFATYYCLOHNSYP
										Section 3
	(103)	103	107							
CUR2-1.6.1_LC	(103)	KVEIK								
A30	(96)	-----								
Consensus	(103)									

FIGURE 24

Figure 24A

							Section 1
	(1)	1	10	20	30	40	51
Cur2-1.11.1_HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
VH3-53	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
Consensus	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
							Section 2
	(52)	52	60	70	80	90	102
Cur2-1.11.1_HC	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
VH3-53	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR-----					
Consensus	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCA					
							Section 3
	(103)	103	110	120			
Cur2-1.11.1_HC	(103)	YYYGMDVWGQETTIVVSS					
VH3-53	(98)	-----					
Consensus	(103)						

Figure 24B

							Section 1
	(1)	1	10	20	30	40	51
CUR2-1.11.1_LC	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLQSN GYN YLDWYLQKPGQSEFQL					
A19	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLH SGN YLDWYLQKPGQSEFQL					
Consensus	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLL SNGYN YLDWYLQKPGQSEFQL					
							Section 2
	(52)	52	60	70	80	90	102
CUR2-1.11.1_LC	(52)	LIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
A19	(52)	LIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTF--					
Consensus	(52)	LIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT					
							Section 3
	(103)	103	111				
CUR2-1.11.1_LC	(103)	GGGTRKVEIK					
A19	(101)	-----					
Consensus	(103)						

FIGURE 25

Figure 25A

									Section 1
	(1)	1	10	20	30	40	51		
CR2-1.17.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFS	SSYGMHWVRQAPGKGLEWVAVI						
VH3-33	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFS	SSYGMHWVRQAPGKGLEWVAVI						
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFS	SSYGMHWVRQAPGKGLEWVAVI						
									Section 2
	(52)	52	60	70	80	90	102		
CR2-1.17.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYC	ARDQGY				
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYC	AR----				
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYC	AR				
									Section 3
	(103)	103	110	126					
CR2-1.17.1_HC	(103)	RYAGYYDY	GMDVMGQGT	TVTVSS					
VH3-33	(99)	-----							
Consensus (103)									

Figure 25B

									Section 1
	(1)	1	10	20	30	40	52		
CR2-1.17.1_LC	(1)	DIQMTQSPSSLSASVGD	RVTTITCRASQGI	RNDLGWYQQKPGKAPKRLTYAAS					
A30	(1)	DIQMTQSPSSLSASVGD	RVTTITCRASQGI	RNDLGWYQQKPGKAPKRLTYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGD	RVTTITCRASQGI	RNDLGWYQQKPGKAPKRLTYAAS					
									Section 2
	(53)	53	60	70	80	90	104		
CR2-1.17.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLT	ISSLPEDFATYYCLQHN	SYPLTFGGG	TKV				
A30	(53)	SLQSGVPSRFSGSGSGTEFTLT	ISSLPEDFATYYCLQHN	SYF-----					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLT	ISSLPEDFATYYCLQHN	SYF					
									Section 3
	(105)	105	107						
CR2-1.17.1_LC	(105)	EIK							
A30	(96)	---							
Consensus	(105)								

FIGURE 26

Figure 26A

						Section 1
	(1)	1	10	20	30	40 52
CR2-1.18_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN				
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN				
						Section 2
	(53)	53	60	70	80	90 104
CR2-1.18_HC	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCAREGLIAVA				
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCAR-----				
Consensus	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCAR				
						Section 3
	(105)	105	110	126		
CR2-1.18_HC	(105)	GTYYYYYGMDVWGQGTITVTVSS				
VH1-8	(99)	-----				
Consensus	(105)					

Figure 26B

							Section 1
	(1)	1	10	20	30	40	53
CR2-1.18_LC	(1)	DIQMTQSPSSISASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS					
A30	(1)	DIQMTQSPSSISASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS					
Consensus	(1)	DIQMTQSPSSISASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS					
							Section 2
	(54)	54	60	70	80	90	106
CR2-1.18_LC	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTRVDI					
A30	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYP-----					
Consensus	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYP					
							Section 3
	(107)	107					
CR2-1.18_LC	(107)	K					
A30	(96)	-					
Consensus	(107)						

FIGURE 27

Figure 27A

							Section 1
	(1)	1	10	20	30	40	52
Cur2-1 19.1 hc	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
							Section 2
	(53)	53	60	70	80	90	104
Cur2-1.19.1 hc	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITF					
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----					
Consensus	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR					
							Section 3
	(105)	105	110	126			
Cur2-1 19.1 hc	(105)	GGVIVHYGMDVWGQGTITVTVSS					
VH1-8	(99)	-----					
Consensus	(105)						

Figure 27B

								Section 1
	(1)	1	10	20	30	40	52	
Cur2-1.19.1 lc	(1)	DIQMTQSPSSLSASVGRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
A30	(1)	DIQMTQSPSSLSASVGRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
Consensus	(1)	DIQMTQSPSSLSASVGRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
								Section 2
	(53)	53	60	70	80	90	104	
Cur2-1.19.1 lc	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFQGQTKL						
A30	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYP-----						
Consensus	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNS P						
								Section 3
	(105)	105	107					
Cur2-1.19.1 lc	(105)	EIR						
A30	(96)	---						
Consensus	(105)							

FIGURE 28

Figure 28A

								Section 1	
	(1)	1	10	20	30	40	51		
Cur2-1.23.1_HC	(1)	EVQLVQSGAEVKKPGESLKISCBGSGYSFTSYWIGWVRQMPGKGLEWMGII							
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCBGSGYSFTSYWIGWVRQMPGKGLEWMGII							
Consensus	(1)	EVQLVQSGAEVKKPGESLKISC GSGYSFTSYWIGWVRQMPGKGLEWMGII							
								Section 2	
	(52)	52	60	70	80	90	102		
Cur2-1.23.1_HC	(52)	YFGDS DTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMYVCARHVS Y							
VH5-51	(52)	YFGDS DTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMYVCAR----							
Consensus	(52)	YFGDS DTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMYVCAR							
								Section 3	
	(103)	103	110	126					
Cur2-1.23.1_HC	(103)	YYVSGSYNVFDYWGQGLVTVSS							
VH5-51	(99)	-----							
Consensus	(103)								

5

Figure 28B

Section 1							
	(1)	10	20	30	40	51	
Cur2-1.23.1 LC	(1)	DIQMTQSPSSSLASVGDRTTITCRASQGIRNDLGWYQQIPGKAPKRLIYAA					
A30	(1)	DIQMTQSPSSSLASVGDRTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPSSSLASVGDRTTITCRASQGIRNDLGWYQQ PGKAPKRLIYAA					
Section 2							
	(52)	60	70	80	90	102	
Cur2-1.23.1 LC	(52)	SSLQGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGQGT					
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----					
Consensus	(52)	SSLQ GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP					
Section 3							
	(103)	103	107				
Cur2-1.23.1 LC	(103)	KVEIK					
A30	(96)	-----					
Consensus	(103)						

10

FIGURE 29

Figure 29A

Section 1					
	(1)	10	20	30	40 51
CR2-1.24.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASG	FSSYGMHWVRQAPGKLEWVADI		
VH3-33	(1)	QVQLVESGGGVVQPGRSLRLSCAASG	FSSYGMHWVRQAPGKLEWVAVI		
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASG	FSSYGMHWVRQAPGKLEWVA I		
Section 2					
	(52)	60	70	80	90 102
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCARDQGY			
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCAR----			
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCAR			
Section 3					
	(103)	110	126		
CR2-1.24.1_HC	(103)	SYGYVYYDYGMDEVWGQGTITVTVSS			
VH3-33	(99)	-----			
Consensus	(103)				

5

Figure 29B

Section 1					
	(1)	10	20	30	40 52
CR2-1.24.1_LC	(1)	DIQMTQSPSSSLASVGVDRVITTCRASQGIRNDLGWYQQKPKAPKRLIYAAS			
A30	(1)	DIQMTQSPSSSLASVGVDRVITTCRASQGIRNDLGWYQQKPKAPKRLIYAAS			
Consensus	(1)	DIQMTQSPSSSLASVGVDRVITTCRASQGIRNDLGWYQQKPKAPKRLIYAAS			
Section 2					
	(53)	60	70	80	90 104
CR2-1.24.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFQGQTKV			
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----			
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP			
Section 3					
	(105)	1067			
CR2-1.24.1_LC	(105)	EIK			
A30	(96)	---			
Consensus	(105)				

10

FIGURE 30

Figure 30A

										Section 1	
		(1)	1	10	20	30	40	51			
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII									
CR2-1.25.1_HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII									
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII									
		(52)	52	60	70	80	90	102			
VH5-51	(52)	YPGDS DTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCAR----									
CR2-1.25.1_HC	(52)	YPGDS DTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCARHGSY									
Consensus	(52)	YPGDS DTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCAR									
		(103)	103	110	126						
VH5-51	(99)	-----									
CR2-1.25.1_HC	(103)	YYGSE TYYNVFDYWGQGLVTVSS									
Consensus	(103)										

Figure 30B

								Section 1
		(1)	1	10	20	30	40	52
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQKPGKAPKRLIYAAS						
CR2-1.25.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQKPGKAPKRLIYAAS						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQKPGKAPKRLIYAAS						
								Section 2
		(53)	53	60	70	80	90	104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP-----						
CR2-1.25.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYPWTFGQGTKV						
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP						
								Section 3
		(105)	1057					
A30	(96)	---						
CR2-1.25.1_LC	(105)	EIK						
Consensus	(105)							

FIGURE 31

Figure 31A

							Section 1
	(1)	1	10	20	30	40	52
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIV					
CR2-1.29_HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIV					
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIV					
							Section 2
	(53)	53	60	70	80	90	104
VH5-51	(53)	PGDS DTRYSPSPFGQQTISADKSISTAYLQWSSLKASDTAMYYCAR-----					
CR2-1.29_HC	(53)	PGDS DTRYSPSPFGQQTISADKSISTAYLQWSSLKASDTAMYYCARHVDVGA					
Consensus	(53)	PGDS DTRYSPSPFGQQTISADKSISTAYLQWSSLKASDTAMYYCAR					
							Section 3
	(105)	105	110	129			
VH5-51	(99)	-----					
CR2-1.29_HC	(105)	TIGGYYYYYHGMDVMGQGTTVTVSS					
Consensus	(105)						

5

Figure 31B

							Section 1
	(1)	1	10	20	30	40	53
A19	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLHSHNGYNYLDWYLQKPGQSPQLLI					
CR2-1.29_LC	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLHSHNGYNYLDWYLQKPGQSPQLLI					
Consensus	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLHSHNGYNYLDWYLQKPGQSPQLLI					
							Section 2
	(54)	54	60	70	80	90	106
A19	(54)	YLGSNRASGVDRFRSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTP-----					
CR2-1.29_LC	(54)	YLGSNRASGVDRFRSGSGSGTDFTLKISRVEAEDVGVVYCMQALQSLMCSFGQ					
Consensus	(54)	YLGSNRASGVDRFRSGSGSGTDFTLKISRVEAEDVGVVYCMQALQS					
							Section 3
	(107)	107	113				
A19	(101)	-----					
CR2-1.29_LC	(107)	GTKLEIK					
Consensus	(107)						

10

FIGURE 32

Figure 32A

								Section 1
	(1)	1	10	20	30	40	52	
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWIS						
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWIS						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWIS						
								Section 2
	(53)	53	60	70	80	90	104	
VH1-18	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----						
CR2-1.33_HC	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYYDS						
Consensus	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR						
								Section 3
	(105)	105	110	127				
VH1-18	(99)	-----						
CR2-1.33_HC	(105)	SDYLYYYYGLDVWGQGTTVTVSS						
Consensus	(105)							

Figure 32B

										Section 1
	(1)	1	10	20	30	40	53			
A20	(1)	DIQMTQSPSSSLASVGDRTTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS								
CR2-1.33_LC	(1)	DIQMTQSPSSSLASVGDRTTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS								
Consensus	(1)	DIQMTQSPSSSLASVGDRTTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS								
										Section 2
	(54)	54	60	70	80	90	106			
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAP-----								
CR2-1.33_LC	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPLTPGGGTKVEI								
Consensus	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAP								
										Section 3
	(107)	107								
A20	(96)	-----								
CR2-1.33_LC	(107)	K								
Consensus	(107)									

FIGURE 33

Figure 33A

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Figure 33B

							Section 1
	(1)	1	10	20	30	40	52
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
CR2-1.38.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVENLLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP LLIYAAS					
							Section 2
	(53)	53	60	70	80	90	104
A20	(53)	TLQSGVPSRFSGSGSGTDFSLTISSLPEDVATYYCQKYNAP-----					
CR2-1.38.1_LC	(53)	TLQSGVPSRFSGSGSGTDFSLTISSLPEDVAAYYCQKCNAPWTFGQGTIV					
Consensus	(53)	TLQSGVPSRFSGSGSGTDFSLTISSLPEDVA YYCQK NSAP					
							Section 3
	(105)	105	107				
A20	(96)	---					
CR2-1.38.1_LC	(105)	EIK					
Consensus	(105)						

FIGURE 34

Figure 34A

									Section 1
	(1)	1	10	20	30	40	51		
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII							
CR2-1.39_1_HC	(1)	EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII							
Consensus	(1)	EVQLVQSG EVKKPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII							
									Section 2
	(52)	52	60	70	80	90	102		
VH5-51	(52)	YPGDS DTRYSPSFQGV TISADKSISTAYLQWSSLKASDTAMY YCAR----							
CR2-1.39_1_HC	(52)	YPGDS DTRYSPSFQGV TISADKSISTAYLQWSSLKASDTAMY YCARHGSY							
Consensus	(52)	YPGDS DTRYSPSFQGV TISADKSISTAYLQWSSLKASDTAMY YCAR							
									Section 3
	(103)	103	110	126					
VH5-51	(99)	-----							
CR2-1.39_1_HC	(103)	YYNSGSYYNVFDYWGGSTLVTVSS							
Consensus	(103)								

5

Figure 34B

							Section 1
	(1)	1	10	20	30	40	52
A30	(1)	DIQMTQS FSSLSASV GDRVTITCRASQ GIRNDLGWYQQKPGKAPKRLIYAAS					
CR2-1.39 1_LC	(1)	DIQMTQS FSSLSASV GDRVTITCRASQ GIRNDLGWYQQKPGKAPKRLIYAAS					
Consensus	(1)	DIQMTQS FSSLSASV GDRVTITCRASQ GIRNDLGWYQQKPGKAPKRLIYAAS					
							Section 2
	(53)	53	60	70	80	90	104
A30	(53)	SLQSGVPSRFS GSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP-----					
CR2-1.39 1_LC	(53)	SLQSGVPSRFS GSGSGTEFTLTIS SLQPEDFATYYCLQHNSYEWTFGQGTKV					
Consensus	(53)	SLQSGVPSRFS GSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP					
							Section 3
	(105)	105	107				
A30	(96)	---					
CR2-1.39 1_LC	(105)	EIK					
Consensus	(105)						

10

FIGURE 35

Figure 35A

								Section 1
	(1)	1	10	20	30	40	52	
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
CR2-1.45_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
								Section 2
	(53)	53	60	70	80	90	104	
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSED TAVYYCAR-----						
CR2-1.45_HC	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSED TAVYYCARGSGYSY						
Consensus	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSED TAVYYCAR						
								Section 3
	(105)	105	110	125				
VH1-8	(99)	-----						
CR2-1.45_HC	(105)	GYDYGGMDVWGQGTTVTVSS						
Consensus	(105)							

Figure 35B

Section 1							
	(1)	1	10	20	30	40	53
A20	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
CR2-1.45_LC	(1)	DIQMTQSPFSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAAS					
Consensus	(1)	DIQMTQSPFSSLSASVGDRVTI CRASQGISN LAWYQQKPGKVPKLLIYAAS					
Section 2							
	(54)	54	60	70	80	90	106
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNSEAP-----					
CR2-1.45_LC	(54)	LQLGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNSEAFPTFGPGTKVDI					
Consensus	(54)	LQ GVPSPRFSGSGSGTDFTLTISLQPEDVATYYCQKYNSEAP					
Section 3							
	(107)	107					
A20	(96)	-					
CR2-1.45_LC	(107)	K					
Consensus	(107)						

FIGURE 36

Figure 36A

		Section 1						
		(1)	1	10	20	30	40	51
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYDINWVRQATGQGLEWMGMN						
CR2-1.46.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYDINWVRQATGQGLEWMGMN						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYSTSYDINWVRQATGQGLEWMGMN						
		Section 2						
		(52)	52	60	70	80	90	102
VH1-8	(52)	NPNSGNTGYAQKFGGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR----						
CR2-1.46.1_HC	(52)	NPNNGNTGYAQKFGGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCARDIVV						
Consensus	(52)	NPN GNTGYAQKFGGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR						
		Section 3						
		(103)	103	110	126			
VH1-8	(99)	-----						
CR2-1.46.1_HC	(103)	VVTATDYYYGMDVWGQGTITVTVSS						
Consensus	(103)							

5

Figure 36B

		Section 1						
		(1)	1	10	20	30	40	52
A30	(1)	DIQMTQSPSSSLASVGDRTTTCRASQGIRNDLGWYQQKPGKAPKRLIFAAAS						
CR2-1.46.1_LC	(1)	DIQMTQSPSSSLASVGDRTTTCRASQGIRNDLGWYQQKPGKAPKRLIFAAAS						
Consensus	(1)	DIQMTQSPSSSLASVGDRTTTCRASQGIRNDLGWYQQKPGKAPKRLIFAAAS						
		Section 2						
		(53)	53	60	70	80	90	104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTITSSLPQPEDFATYYCLQHNSTYP-----						
CR2-1.46.1_LC	(53)	SLPSGVPSRFSGSGSGTEFTLTITSSLPQPEDFATYYCLQHSGYPTTFGQGTKV						
Consensus	(53)	SL SGVPSRFSGSGSGTEFTLTITSSLPQPEDFATYYCLQH YP						
		Section 3						
		(105)	1057					
A30	(96)	---						
CR2-1.46.1_LC	(105)	EIK						
Consensus	(105)							

10

FIGURE 37

Figure 37A

						Section 1
	(1)	1	10	20	30	40 51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI				
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI				
						Section 2
	(52)	52	60	70	80	90 102
CR2-1.48.1_HC	(52)	SAYNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCARDVEY				
VH1-18	(52)	SAYNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCAR----				
Consensus	(52)	SAYNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCAR				
						Section 3
	(103)	103	110	125		
CR2-1.48.1_HC	(103)	YYDGSGLYYFDYWGQGLTVTVSS				
VH1-18	(99)	-----				
Consensus	(103)					

Figure 37B

						Section 1
	(1)	1	10	20	30	40 52
CR2-1.48.1_LC	(1)	DIQMTQSPSSVSASVGDRVTTTCRASQGISSWLAWYQQKPGKAPKLLIYAAS				
L5	(1)	DIQMTQSPSSVSASVGDRVTTTCRASQGISSWLAWYQQKPGKAPKLLIYAAS				
Consensus	(1)	DIQMTQSPSSVSASVGDRVTTTCRASQGISSWLAWYQQKPGKAPKLLIYAAS				
						Section 2
	(53)	53	60	70	80	90 104
CR2-1.48.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYCQQANSFRTFGQGTKV				
L5	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYCQQANSFP-----				
Consensus	(53)	LQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYCQQANSFP				
						Section 3
	(105)	105				
CR2-1.48.1_LC	(105)	EIK				
L5	(96)	---				
Consensus	(105)					

FIGURE 38

Figure 38A

Section 1					
	(1)	1	10	20	30 40 51
CR2-1.49.1 HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM			
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM			
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM			
Section 2					
	(52)	52	60	70	80 90 102
CR2-1.49.1 HC	(52)	NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDI			
VH1-8	(52)	NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR----			
Consensus	(52)	NPNSG TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR			
Section 3					
	(103)	103	110	127	
CR2-1.49.1 HC	(103)	VATSYYYYFYGMDEVGQGTFTVTS			
VH1-8	(99)	-----			
Consensus	(103)				

Figure 38B

Section 1					
	(1)	1	10	20	30 40 52
CR2-1.49.1_LC	(1)	DIVMTQSELSLPVTPGEPASISCRSSQSLLHNSNGYNYLDWYLLKPGQSPQLL			
A19	(1)	DIVMTQSELSLPVTPGEPASISCRSSQSLLHNSNGYNYLDWYLLKPGQSPQLL			
Consensus	(1)	DIVMTQSELSLPVTPGEPASISCRSSQSLLHNSNGYNYLDWYL KPGQSPQLL			
Section 2					
	(53)	53	60	70	80 90 104
CR2-1.49.1_LC	(53)	IYLGSSRASGVFDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQTITFGQ			
A19	(53)	IYLGSNRASGVFDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP----			
Consensus	(53)	IYLGSRASGVFDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ LQT			
Section 3					
	(105)	105	111		
CR2-1.49.1_LC	(105)	GTRLEIK			
A19	(101)	-----			
Consensus	(105)				

FIGURE 39

Figure 39A

Section 1						
	(1)	1	10	20	30 40 51	
CR2-1.51.1_HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
Section 2						
	(52)	52	60	70	80 90 102	
CR2-1.51.1_HC	(52)	YPGDSDAKYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYTCARHYDY				
VH5-51	(52)	YPGDSDTKYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYTCAR----				
Consensus	(52)	YPGDSD KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYTCAR				
Section 3						
	(103)	103	110	126		
CR2-1.51.1_HC	(103)	VWRNRYRTGWFDPWGQGLTVVSS				
VH5-51	(99)	-----				
Consensus	(103)					

Figure 39B

						Section 1	
	(1)	1	10	20	30	40	52
CR2-151.1_LC	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGA					
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGA					
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGA					
						Section 2	
	(53)	53	60	70	80	90	104
CR2-151.1_LC	(53)	SNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLPFTFGPGTK					
A27	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-----					
Consensus	(53)	S RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS					
						Section 3	
	(105)	10508					
CR2-151.1_LC	(105)	VDIK					
A27	(97)	----					
Consensus	(105)						

FIGURE 40

Figure 40A

									Section 1
	(1)	1	10	20	30	40	52		
Cur2-6.4.1_hc	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN							
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN							
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN							
									Section 2
	(53)	53	60	70	80	90	104		
Cur2-6.4.1_hc	(53)	PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRFGFGYSY							
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAIYYCAR-----							
Consensus	(53)	PNSGNT YAQKFQGRVTMTR TSISTAYMELSSLRSEDTAIYYC R							
									Section 3
	(105)	105	110	125					
Cur2-6.4.1_hc	(105)	NYDYYYGMDVWGQGTITVTVSS							
VH1-8	(99)	-----							
Consensus	(105)								

Figure 40B

							Section 1
	(1)	1	10	20	30	40	52
Cur2-6.4.1_Lc	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYAT					
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYSA					
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYA					
							Section 2
	(53)	53	60	70	80	90	104
Cur2-6.4.1_Lc	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGQTK					
A27	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-----					
Consensus	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP					
							Section 3
	(105)	105	108				
Cur2-6.4.1_Lc	(105)	LEIK					
A27	(97)	----					
Consensus	(105)						

FIGURE 41

CLONE #	VH	#DE L	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.19.1	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
1.19.2	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
1.19.3	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)

CLONE	vk	#de 1	vk end	#n	N SEQ	Jk	# del	JK end
-------	----	-------	--------	----	-------	----	-------	--------

1.19.1	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.2	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.3	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
6.4.1	A27/A27A	-3	CTCACC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)

ABX-Cur2 pat app.1

	A27/A27A	-3	NO:101)		NO:102)			NO:103)
6.4.2	A27/A27A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTGG (SEQ ID NO:103)

FIGURE 42

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.11.2	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)

CLONE	Vk	#del	vk end	#n	N SEQ	JK	# del	JK end
1.6.1	A30	-3	TTACCC (SEQ ID NO:104)	0	0	JK4	0	GCTCACT (SEQ ID NO:107)

1.6.2	A30	-3	NO:116) TTACCC (SEQ ID NO:116)	0	0	JK4	0	NO:117) GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)

FIGURE 43

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D6-19	19	GGGTATAG CAGTGGCT GG (SEQ ID NO:126)	4	GACA	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.25.1	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTATTA TGGTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:135)

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTA TGGTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:134)
1.29	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTGGATgT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT (SEQ ID NO:137)	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaaTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.39.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaaTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.40.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:147)	0	0	D2	25	ATATTGTA GTGGTGGT	2	CA	JH6B	-6	ACTACT (SEQ ID NO:150)

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
			NO:151)					AGCTGCTA C (SEQ ID NO:152)					NO:153)
1.40.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-15/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GGTGGTA GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGa GGAAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGa GGAAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)

CLONE	vk	#del	vk end	#n	N SEQ	Jk	# del	JK end
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1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
1.18	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK3	0	ATTACAC (SEQ ID NO:173)
1.24.1	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK1	0	GTGGAC (SEQ ID NO:175)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.25.1	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:180)	0	0	JK1	0	GTGGAC (SEQ ID NO:181)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:182)	14	TCTCTCATG TGCAG (SEQ ID NO:183)	JK2	-7	TTTTGG (SEQ ID NO:184)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK4	0	GCTCAC (SEQ ID NO:186)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.39.1	A30	3	TTACCC (SEQ ID NO:189)	0	0	JK1	0	GTGGAC (SEQ ID NO:190)
1.39.2	A30	3	TTACCC (SEQ ID NO:191)	0	0	JK1	0	ATTACAC (SEQ ID NO:192)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:193)	0	0	JK3	0	ATTACAC (SEQ ID NO:194)
1.46.1	A30	0	CCCTCC (SEQ ID NO:195)	0	0	JK1	-3	GACGTT (SEQ ID NO:196)

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
			NO:191)					NO:192)
1.46.2	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.48.1	L5/DPK5/V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.48.2	L5/DPK5/V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.49.2	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)

FIGURE 44

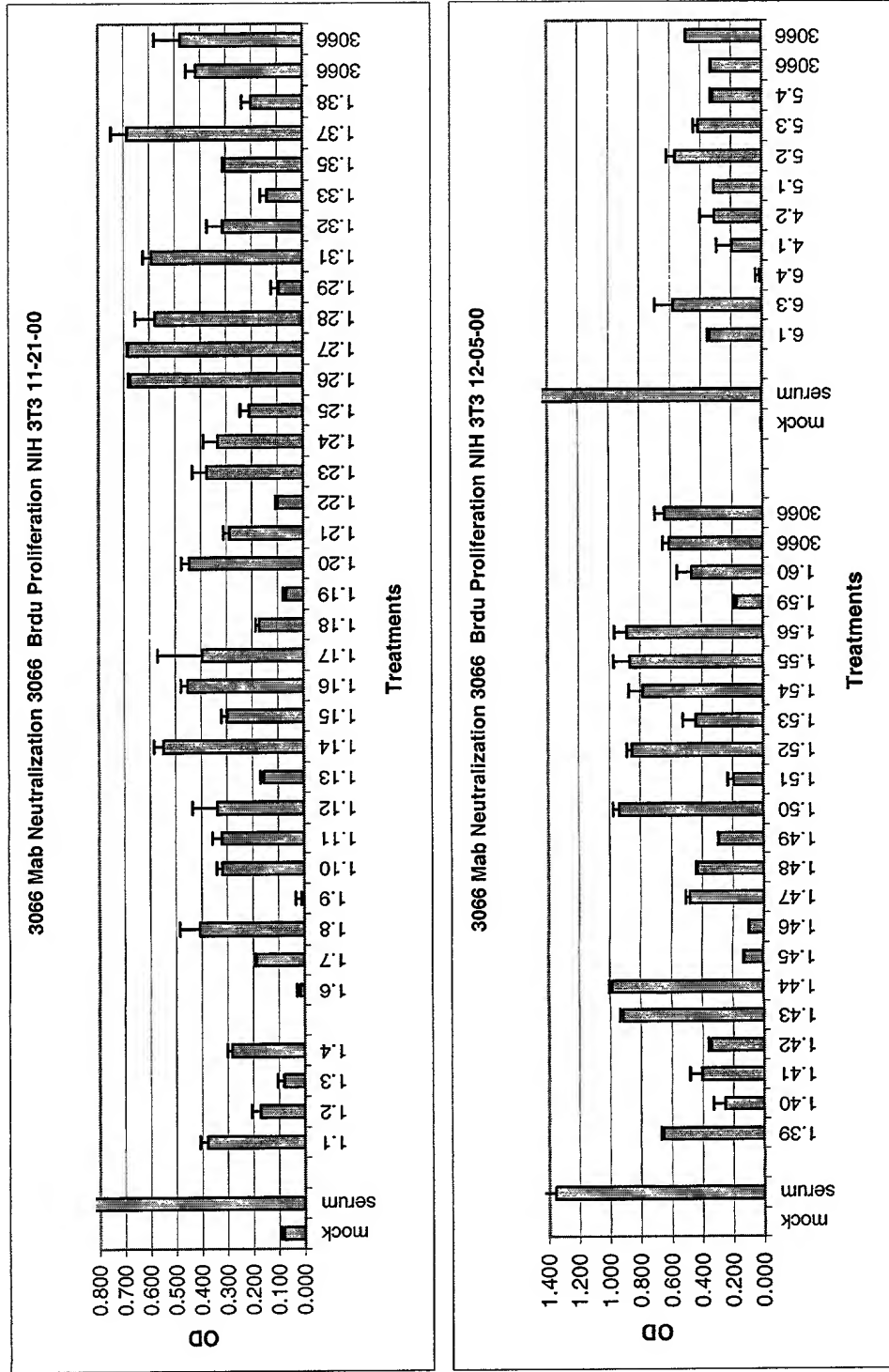
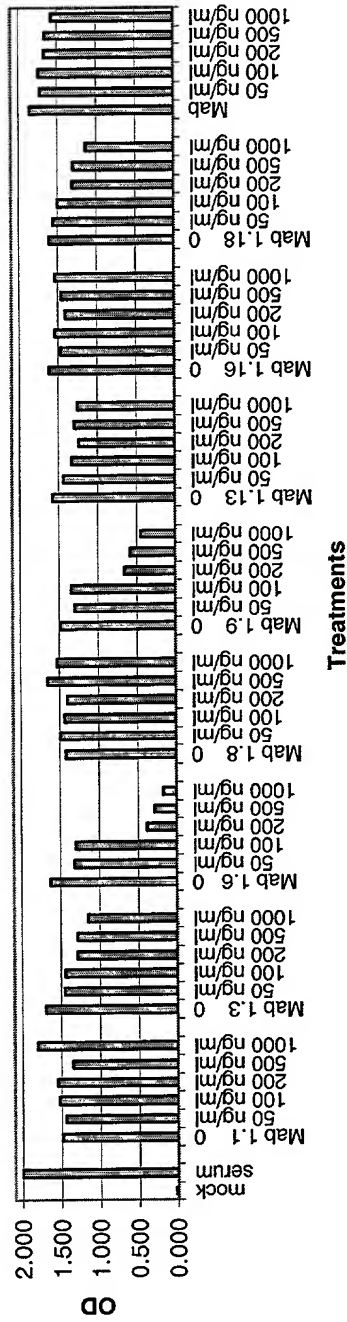
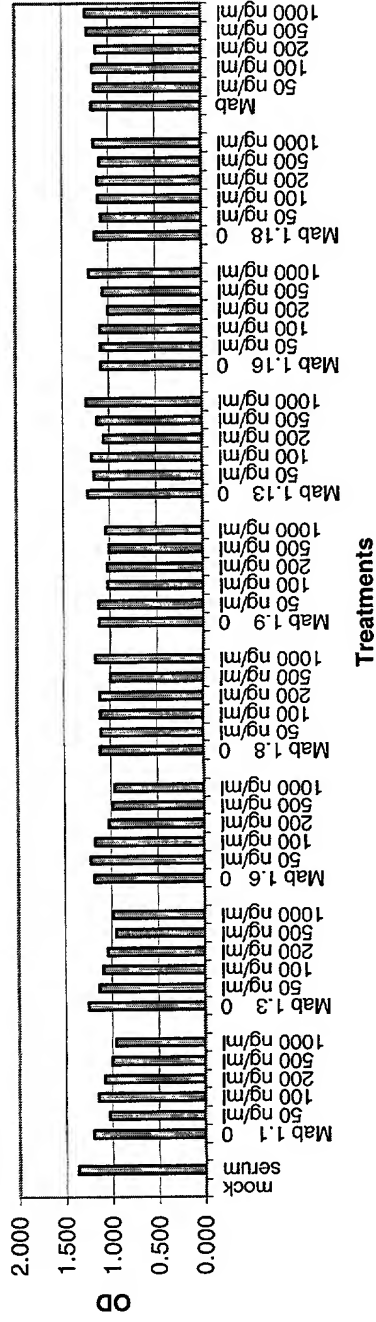


FIGURE 45

3066 Mab Neutralization 3066 Brdu Proliferation NIH 3T3 11-22-00



3066 Mab Neutralization PDGF BB Brdu Proliferation NIH 3T3 11-22-00



[illegible]

FIGURE 47

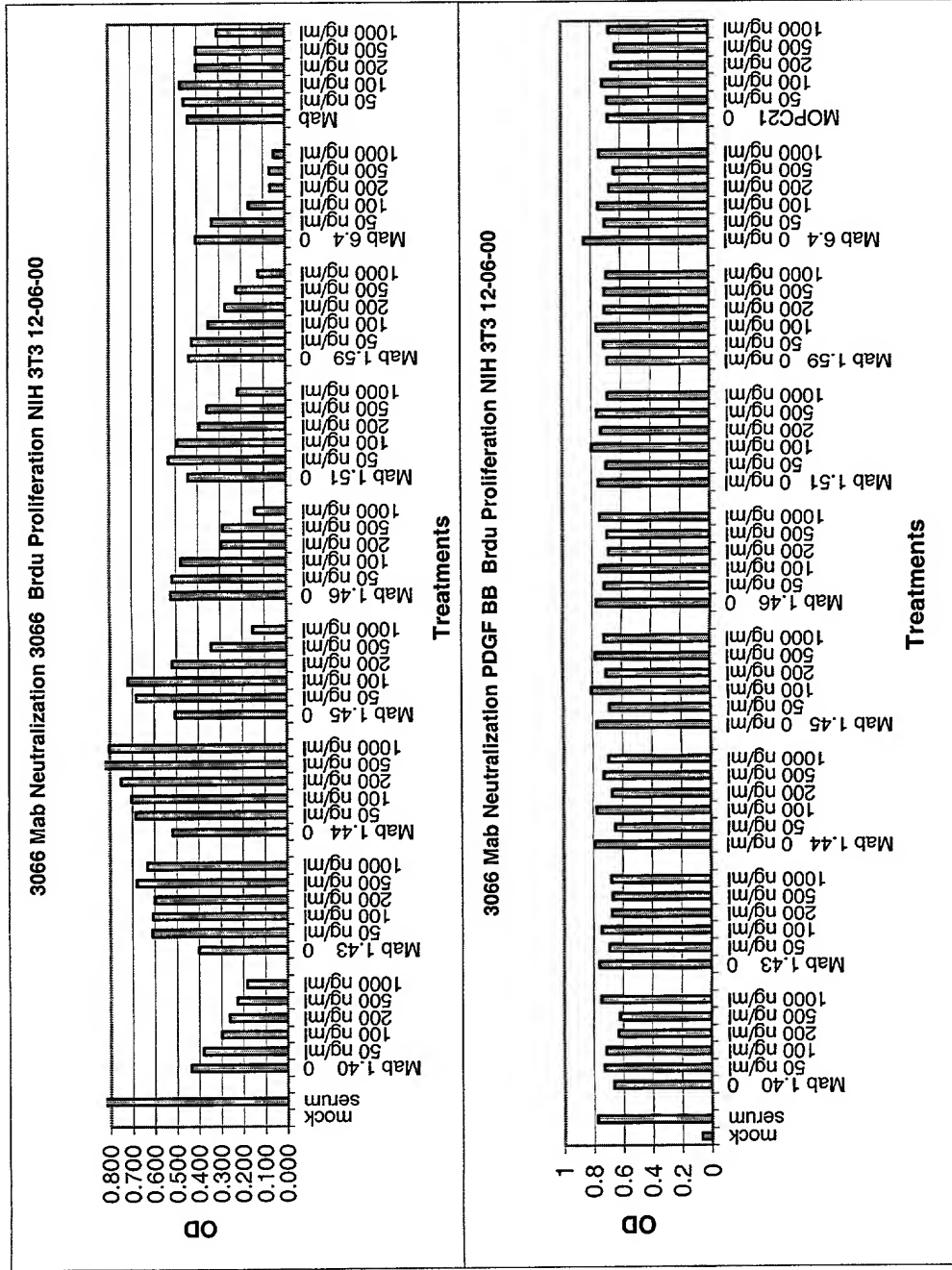


FIGURE 48

1.19 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
6.4 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTDY	60
1.18 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.40 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.45 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.46 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.49 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.33 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
1.48 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
1.6 H	1	EVQLVESGGGLVKKPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSSISSSSSSNIYY	60
1.17 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDGNSKYY	60
1.24 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDGNSKYY	60
1.38 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDGNSKYY	60
1.11 H	1	EVQLVQSGGGGLIQQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGS-TYY	59
1.23 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIITYPGDSITRY	60
1.25 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIITYPGDSITRY	60
1.29 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIITYPGDSITRY	60
1.39 H	1	EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIITYPGDSITRY	60
1.51 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIITYPGDSITRY	60
		[____CDR1____]	[____CDR2____]
1.19 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--DVM-ITFGGVIVH-YGMDVW	116
6.4 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--GFG-YSYN-YDYY-YGMDVW	115
1.18 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--EG--IAVAGTYYYYGYMDVW	116
1.40 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--DIV-VVVAATNYY-NGMDVW	116
1.45 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--GSG-YSYG-YDYY-YGMDVW	115
1.46 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--DIV-VVVTATDYY-YGMDVW	116
1.49 H	61	AQKFQGRVTMTIRNTSISTAYMELSSLRSEDATAVYYCAR--MRD-IVATSYYYYFYGMDVW	117
1.33 H	61	AQKLQGRVTMTITSTSTAYMELSSLRSEDATAVYYCAR--DHY-YDSSDYLYYYYGLDVGW	117
1.48 H	61	AQKLQGRVTMTITSTSTAYMELSSLRSEDATAVYYCARDVEYY-YDGSYYYFDY----W	115
1.6 H	61	ADSVKGRFTISRDNAKNSLYLQMNSLRSEDATAVYYCARDIMI---TFG-GIIASFYFDYW	116
1.17 H	61	ADSVKGRFTISRDNSKNTLYLQMNSLRSEDATAVYYCARDQGY---RYA-GYYDYGYMDVW	116
1.24 H	61	ADSVKGRFTISRDNSKNTLYLQMNSLRSEDATAVYYCARDQGY---SYG-YVYDYGYMDVW	116
1.38 H	61	ADSVKGRFTISRDNSKNTLYLQMNSLRSEDATAVYYCARGYYD--SSD-YLYYYYGYMDVW	117
1.11 H	60	ADSVKGRFTISRDNSKNTLYLQMNSLRSEDATAVYYCAGTVTT-----NYYYGYMDVW	110
1.23 H	61	SPSFQGGVTTISADKSISTAYLQWSSLKASDTAMYYCARHVSY---YVSGSY-NVFDYW	116
1.25 H	61	SPSFQGGVTTISADKSISTAYLQWSSLKASDTAMYYCARHGSY---YVGSETYY-NVFDYW	116
1.29 H	61	SPSFQGGVTTISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYY-HGMDVW	119
1.39 H	61	SPSFQGGVTTISADKSISTAYLQWSSLKASDTAMYYCARHGSY---YVSGSY-NVFDYW	116
1.51 H	61	SPSFQGGVTTISADKSISTAYLQWSSLKASDTAMYYCARHYDY---VWRNYRYT-GWFDPW	116
		[____CDR3____]	

FIGURE 48 (CONT)

1.19 H	117	GQGTIVTVSS	126
6.4 H	116	GQGTIVTVSS	125
1.18 H	117	GQGTIVTVSS	126
1.40 H	117	GQGTIVTVSS	126
1.45 H	116	GQGTIVTVSS	125
1.46 H	117	GQGTIVTVSS	126
1.49 H	118	GQGTIVTVSS	127
1.33 H	118	GQGTIVTVSS	127
1.48 H	116	GQGTIVTVSS	125
1.6 H	117	GQGTIVTVSS	126
1.17 H	117	GQGTIVTVSS	126
1.24 H	117	GQGTIVTVSS	126
1.38 H	118	GQGTIVTVSS	127
1.11 H	111	GQGTIVTVSS	120
1.23 H	117	GQGTIVTVSS	126
1.25 H	117	GQGTIVTVSS	126
1.29 H	120	GQGTIVTVSS	129
1.39 H	117	GQGTIVTVSS	126
1.51 H	117	GQGTIVTVSS	126

FIGURE 49

1.48 L	1	DIQMTQSPSSVSASVGDRVTITCRASQGIS	SS-----WLA	WYQQKPGKAPKLLIYAASILQ	55
1.49 L	1	DIVMTQSPPLSLPVTPGEPASISCRSSQSLH	SNGYNYLDWYLLKPGQSPQLLIYLGSSRA	60	
1.11 L	1	DIVMTQSPPLSLPVTPGEPASISCRSSQSLH	SNGYNYLDWYLLKPGQSPQLLIYLGSSRA	60	
1.29 L	1	DIVMTQSPPLSLPVTPGEPASISCRSSQSLH	SNGYNYLDWYLLKPGQSPQLLIYLGSSRA	60	
1.45 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIS	SN-----DLA	WYQQKPGKVPKLLIYAASILQ	55
1.33 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIS	SN-----YLA	WYQQKPGKVPKLLIYAASILQ	55
1.38 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIS	SN-----YLA	WYQQKPGKVPNLLIYAASILQ	55
6.4 L	1	EIVLTQSPGTLISLSPGERATLSCRASQSVSS	SS-----YLA	WYQQKPGQAPRLLIYATSSRA	56
1.51 L	1	EIVLTQSPGTLISLSPGERATLSCRASQSVSS	SS-----YLA	WYQQKPGQAPRLLIYATSSRA	56
1.19 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.18 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.16 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.23 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.25 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.39 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.17 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.24 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILQ	55
1.46 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRN	-----DLG	WYQQKPGKAPKRLIYAASILP	55

[CDR1]

[CDR2]

1.48 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	SYCQSN	SFPT	FGQGTKVEIK	107
1.49 L	61	SGVPDRFGSGSGTDFTLTKISRVEAEDVG	VYCMQTLQ	TIT--	FGQGTKVEIK	111
1.11 L	61	SGVPDRFGSGSGTDFTLTKISRVEAEDVG	VYCMQALQ	TIT--	FGQGTKVEIK	111
1.29 L	61	SGVPDRFGSGSGTDFTLTKISRVEAEDVG	VYCMQALQ	SLMCS	FGQGTKVEIK	113
1.45 L	56	LGVPSRFGSGSGTDFTLTISSLOPEDVA	TYCQKYN	SAPFT	FGPGTKVEIK	107
1.33 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDVA	TYCQKYN	SAPLT	FGQGTKVEIK	107
1.38 L	56	SGVPSRFGSGSGTDFSLTISSLOPEDVA	AAYCQKC	NAPWT	FGQGTKVEIK	107
6.4 L	57	IGIPDRFGSGSGTDFTLTISRLEPEDFA	VYCYGSS	SPCS	FGQGTKVEIK	108
1.51 L	57	IGIPDRFGSGSGTDFTLTISRLEPEDFA	VYCYGSS	SLFT	FGPGTKVEIK	108
1.19 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	DPCT	FGQGTKVEIK	107
1.18 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPFT	FGPGTKVEIK	107
1.16 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPLT	FGQGTKVEIK	107
1.23 L	56	RGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPWT	FGQGTKVEIK	107
1.25 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPWT	FGQGTKVEIK	107
1.39 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPWT	FGQGTKVEIK	107
1.17 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPWT	FGQGTKVEIK	107
1.24 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	YPWT	FGQGTKVEIK	107
1.46 L	56	SGVPSRFGSGSGTDFTLTISSLOPEDFA	TYCLOHNS	GPPT	FGQGTKVEIK	107

[]

[CDR3]

FIGURE 50

1.19 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
6.4 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTDY	60
1.18 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.40 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.45 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.46 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.49 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60

[CDR1] [CDR2]

1.19 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	119
6.4 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	118
1.18 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	119
1.40 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	119
1.45 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	118
1.46 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	119
1.49 H	61	AQKFQGRVTMTNRNTSISTAYMELSSLRSED TAVYYCARDVMITFGG-VIVYGM	120

[CDR3]

1.19 H	120	TTVTVSS	126
6.4 H	119	TTVTVSS	125
1.18 H	120	TTVTVSS	126
1.40 H	120	TTVTVSS	126
1.45 H	119	TTVTVSS	125
1.46 H	120	TTVTVSS	126
1.49 H	121	TTVTVSS	127

FIGURE 51

1.33 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
1.48 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
		[____CDR1____]	[____CDR2____]
1.33 H	61	AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DYDSSDYLYYYYGLDVWG	118
1.48 H	61	AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYDGSGLYYEDY-----WG	116
		[____CDR3____]	
1.33 H	119	QGTITVTVSS	127
1.48 H	117	QGTITVTVSS	125

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DYDSSDYLYYYYGLDVWG
AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYDGSGLYYEDY-----WG
QGTITVTVSS
QGTITVTVSS

FIGURE 52

1.17 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFS	SSYGMHWVRQAPGKGLEWVA	IWYDGSNKYY	60
1.24 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFS	SSYGMHWVRQAPGKGLEWVA	IWYDGSNKYY	60
1.38 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFS	SSYGMHWVRQAPGKGLEWVA	IWYDGSNKYY	60
		[CDR1]			[CDR2]
1.17 H	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY	-RYAGY	YDYGMDVWGQG	119
1.24 H	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY	-SYGYV	YDYGMDVWGQG	119
1.38 H	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYY	DSSDYL	YDYGMDVWGQG	120
		[CDR3]			
1.17 H	120	TTVTVSS	126		
1.24 H	120	TTVTVSS	126		
1.38 H	121	TTVTVSS	127		

QVQLVESGGGVVQPGKSLRLSCAASGFTFS
SSYGMHWVRQAPGKGLEWVAIWYDGSNKYY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY
-RYAGY YDYGMDVWGQG
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYY
DSSDYL YDYGMDVWGQG
TTVTVSS

FIGURE 53

1.23 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY	60
1.25 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY	60
1.29 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY	60
1.39 H	1	EVQLVQSGTIEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY	60
1.51 H	1	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDS DAKY	60

[____CDR1____]

[____CDR2____]

1.23 H	61	SPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYYVSG---SYYNVFDYWG	117
1.25 H	61	SPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSE---TYYNVFDYWG	117
1.29 H	61	SPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYTGMDVWG	120
1.39 H	61	SPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYNSG---SYYNVFDYWG	117
1.51 H	61	SPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCARHYDYVVRNY---RYTGWFDPWG	117

[____CDR3____]

1.23 H	118	QGT LVT VSS	126
1.25 H	118	QGT LVT VSS	126
1.29 H	121	QGT LVT VSS	129
1.39 H	118	QGT LVT VSS	126
1.51 H	118	QGT LVT VSS	126

FIGURE 54

1.49 L	1	DIVMTQSPLSLPVT	PGEPA	ISCRSSQSL	LH	SNGYNYLDWYL	L	KPGQSPQLLIYLGSSRA	60
1.11 L	1	DIVMTQSPLSLPVT	PGEPA	ISCRSSQSL	LQ	SNGYNYLDWYL	L	KPGQSPQLLIYLGSNRA	60
1.29 L	1	DIVMTQSPLSLPVT	PGEPA	ISCRSSQSL	LH	SNGYNYLDWYL	L	KPGQSPQLLIYLGSNRA	60
				[CDR1]				[CDR2]	
1.49 L	61	SGVPDRFSGSGSGT	DFTL	KISRVEA	EDVG	VYYCMQ	TLOT	IT--FGQ	TRLEIK 111
1.11 L	61	SGVPDRFSGSGSGT	DFTL	KISRVEA	EDVG	VYYCMQ	ALQT	IT--FGG	TKVEIK 111
1.29 L	61	SGVPDRFSGSGSGT	DFTL	KISRVEA	EDVG	VYYCMQ	ALQSL	MCSEFGQ	TKLEIK 113
				[CDR3]					

1.49 L 1 DIVMTQSPLSLPVT PGEPA ISCRSSQSL LH SNGYNYLDWYL L KPGQSPQLLIYLGSSRA 60
1.11 L 1 DIVMTQSPLSLPVT PGEPA ISCRSSQSL LQ SNGYNYLDWYL L KPGQSPQLLIYLGSNRA 60
1.29 L 1 DIVMTQSPLSLPVT PGEPA ISCRSSQSL LH SNGYNYLDWYL L KPGQSPQLLIYLGSNRA 60
[CDR1] [CDR2]
1.49 L 61 SGVPDRFSGSGSGT DFTL KISRVEA EDVG VYYCMQ TLOT IT--FGQ TRLEIK 111
1.11 L 61 SGVPDRFSGSGSGT DFTL KISRVEA EDVG VYYCMQ ALQT IT--FGG TKVEIK 111
1.29 L 61 SGVPDRFSGSGSGT DFTL KISRVEA EDVG VYYCMQ ALQSL MCSEFGQ TKLEIK 113
[CDR3]

FIGURE 55

1.45 L	1	DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQLGVPS	60
1.33 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS	60
1.38 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQSGVPS	60
		[___CDR1___]	[_CDR2_]
1.45 L	61	RFSGSGSGTDFILTISSLQPEDVATYYCQKYNAPFTFGPGTKVDIK	107
1.33 L	61	RFSGSGSGTDFILTISSLQPEDVATYYCQKYNAPLTFGGGTKEIK	107
1.38 L	61	RFSGSGSGTDFSLTISSLQPEDVAAYYCQKCNAPWTFGQGTVEIK	107
		[___CDR3___]	

DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQLGVPS 60
DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQSGVPS 60
[___CDR1___] [_CDR2_] 60
RFSGSGSGTDFILTISSLQPEDVATYYCQKYNAPFTFGPGTKVDIK 107
RFSGSGSGTDFILTISSLQPEDVATYYCQKYNAPLTFGGGTKEIK 107
RFSGSGSGTDFSLTISSLQPEDVAAYYCQKCNAPWTFGQGTVEIK 107
[___CDR3___] 107

FIGURE 56

6.4 L	1	EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSSRATGIP	60
1.51 L	1	EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP	60
		[___CDR1___]	[___CDR2___]
6.4 L	61	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGQTKLEIK	108
1.51 L	61	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFIFGPGTKVDIK	108
		[___CDR3___]	

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FIGURE 57

1.19 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.18 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.16 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.23 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.25 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.39 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.17 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.24 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.46 L	1	DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60

[___CDR1___] [___CDR2___]

1.19 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSDPCSFQGGTKLEIR	107
1.18 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPFTFGPGTKVEIK	107
1.16 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK	107
1.23 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK	107
1.25 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK	107
1.39 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK	107
1.17 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK	107
1.24 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK	107
1.46 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSGYPPTFGGGTKVEIK	107

[___CDR3___]